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RAW SEQUENCE LISTING

DATE: 08/29/2003

PATENT APPLICATION: US/09/974,973A

TIME: 14:45:48

Input Set : A:\subseqlist 1533_1230001.txt

Output Set: N:\CRF4\08292003\I974973A.raw

5 <110> APPLICANT: Hanke, Paul D.
 9 <120> TITLE OF INVENTION: Feedback-Resistant Pyruvate Carboxylase Gene from Corynebacterium
 13 <130> FILE REFERENCE: 1533.1230001
 17 <140> CURRENT APPLICATION NUMBER: US 09/974,973A
 19 <141> CURRENT FILING DATE: 2001-10-12
 23 <150> PRIOR APPLICATION NUMBER: US 60/239,913
 25 <151> PRIOR FILING DATE: 2000-10-13
 29 <160> NUMBER OF SEQ ID NOS: 19
 33 <170> SOFTWARE: PatentIn version 3.0
 37 <210> SEQ ID NO: 1
 39 <211> LENGTH: 3474
 41 <212> TYPE: DNA
 43 <213> ORGANISM: Corynebacterium glutamicum
 47 <220> FEATURE:
 49 <221> NAME/KEY: CDS
 51 <222> LOCATION: (1)..(3474)
 55 <400> SEQUENCE: 1
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 57 Met Thr Ala Ile Thr Leu Gly Gly Leu Leu Leu Lys Gly Ile Ile Thr
 58 1 5 10 15
 60 cta gtg tcg act cac aca tct tca acg ctt cca gca ttc aaa aag atc 96
 61 Leu Val Ser Thr His Thr Ser Ser Thr Leu Pro Ala Phe Lys Lys Ile
 62 20 25 30
 64 ttg gta gca aac cgc ggc gaa atc gcg gtc cgt gct ttc cgt gca gca 144
 65 Leu Val Ala Asn Arg Gly Glu Ile Ala Val Arg Ala Phe Arg Ala Ala
 66 35 40 45
 68 ctc gaa acc ggt gca gcc acg gta gct att tac ccc cgt gaa gat cgg 192
 69 Leu Glu Thr Gly Ala Ala Thr Val Ala Ile Tyr Pro Arg Glu Asp Arg
 70 50 55 60
 72 gga tca ttc cac cgc tct ttt gct tct gaa gct gtc cgc att ggt act 240
 73 Gly Ser Phe His Arg Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr
 74 65 70 75 80
 76 gaa ggc tca cca gtc aag gcg tac ctg gac atc gat gaa att atc ggt 288
 77 Glu Gly Ser Pro Val Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Gly
 78 85 90 95
 80 gca gct aaa aaa gtt aaa gca gat gct att tac ccg gga tat ggc ttc 336
 81 Ala Ala Lys Lys Val Lys Ala Asp Ala Ile Tyr Pro Gly Tyr Gly Phe
 82 100 105 110
 84 ctg tct gaa aat gcc cag ctt gcc cgc gag tgc gcg gaa aac ggc att 384
 85 Leu Ser Glu Asn Ala Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Ile
 86 115 120 125
 88 act ttt att ggc cca acc cca gag gtt ctt gat ctc acc ggt gat aag 432
 89 Thr Phe Ile Gly Pro Thr Pro Glu Val Leu Asp Leu Thr Gly Asp Lys

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92 tct cgt gcg gta acc gcc gcg aag aag gct ggt ctg cca gtt ttg gcg      480
93 Ser Arg Ala Val Thr Ala Ala Lys Lys Ala Gly Leu Pro Val Leu Ala
94 145      150      155      160
96 gaa tcc acc ccg agc aaa aac atc gat gac atc gtt aaa agc gct gaa      528
97 Glu Ser Thr Pro Ser Lys Asn Ile Asp Asp Ile Val Lys Ser Ala Glu
98      165      170      175
100 ggc cag act tac ccc atc ttt gta aag gca gtt gcc ggt ggt ggc gga      576
101 Gly Gln Thr Tyr Pro Ile Phe Val Lys Ala Val Ala Gly Gly Gly Gly
102      180      185      190
104 cgc ggt atg cgc ttt gtt tct tca cct gat gag ctc cgc aaa ttg gca      624
105 Arg Gly Met Arg Phe Val Ser Ser Pro Asp Glu Leu Arg Lys Leu Ala
106      195      200      205
108 aca gaa gca tct cgt gaa gct gaa gcg gca ttc ggc gac ggt tgc gta      672
109 Thr Glu Ala Ser Arg Glu Ala Glu Ala Ala Phe Gly Asp Gly Ser Val
110      210      215      220
112 tat gtc gaa cgt gct gtg att aac ccc cag cac att gaa gtg cag atc      720
113 Tyr Val Glu Arg Ala Val Ile Asn Pro Gln His Ile Glu Val Gln Ile
114 225      230      235      240
116 ctt ggc gat cgc act gga gaa gtt gta cac ctt tat gaa cgt gac tgc      768
117 Leu Gly Asp Arg Thr Gly Glu Val Val His Leu Tyr Glu Arg Asp Cys
118      245      250      255
120 tca ctg cag cgt cgt cac caa aaa gtt gtc gaa att gcg cca gca cag      816
121 Ser Leu Gln Arg Arg His Gln Lys Val Val Glu Ile Ala Pro Ala Gln
122      260      265      270
124 cat ttg gat cca gaa ctg cgt gat cgc att tgt gcg gat gca gta aag      864
125 His Leu Asp Pro Glu Leu Arg Asp Arg Ile Cys Ala Asp Ala Val Lys
126      275      280      285
128 ttc tgc cgc tcc att ggt tac cag ggc gcg gga acc gtg gaa ttc ttg      912
129 Phe Cys Arg Ser Ile Gly Tyr Gln Gly Ala Gly Thr Val Glu Phe Leu
130      290      295      300
132 gtc gat gaa aag ggc aac cac gtt ttc atc gaa atg aac cca cgt atc      960
133 Val Asp Glu Lys Gly Asn His Val Phe Ile Glu Met Asn Pro Arg Ile
134 305      310      315      320
136 cag gtt gag cac acc gtg act gaa gaa gtc acc gag gtg gac ctg gtg      1008
137 Gln Val Glu His Thr Val Thr Glu Glu Val Thr Glu Val Asp Leu Val
138      325      330      335
140 aag gcg cag atg cgc ttg gct gct ggt gca acc ttg aag gaa ttg ggt      1056
141 Lys Ala Gln Met Arg Leu Ala Ala Gly Ala Thr Leu Lys Glu Leu Gly
142      340      345      350
144 ctg acc caa gat aag atc aag acc cac ggt gca gca ctg cag tgc cgc      1104
145 Leu Thr Gln Asp Lys Ile Lys Thr His Gly Ala Ala Leu Gln Cys Arg
146      355      360      365
148 atc acc acg gaa gat cca aac aac ggc ttc cgc cca gat acc gga act      1152
149 Ile Thr Thr Glu Asp Pro Asn Asn Gly Phe Arg Pro Asp Thr Gly Thr
150      370      375      380
152 atc acc gcg tac cgc tca cca ggc gga gct ggc gtt cgt ctt gac ggt      1200
153 Ile Thr Ala Tyr Arg Ser Pro Gly Gly Ala Gly Val Arg Leu Asp Gly
154 385      390      395      400

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156	gca gct cag ctc ggt ggc gaa atc acc gca cac ttt gac tcc atg ctg	1248
157	Ala Ala Gln Leu Gly Gly Glu Ile Thr Ala His Phe Asp Ser Met Leu	
158	405 410 415	
160	gtg aaa atg acc tgc cgt ggt tcc gac ttt gaa act gct gtt gct cgt	1296
161	Val Lys Met Thr Cys Arg Gly Ser Asp Phe Glu Thr Ala Val Ala Arg	
162	420 425 430	
164	gca cag cgc gcg ttg gct gag ttc acc gtg tct ggt gtt gca acc aac	1344
165	Ala Gln Arg Ala Leu Ala Glu Phe Thr Val Ser Gly Val Ala Thr Asn	
166	435 440 445	
168	att ggt ttc ttg cgt gcg ttg ctg cgg gaa gag gac ttc act tcc aag	1392
169	Ile Gly Phe Leu Arg Ala Leu Leu Arg Glu Glu Asp Phe Thr Ser Lys	
170	450 455 460	
172	cgc atc gcc acc gga ttt atc ggc gat cac cca cac ctc ctt cag gct	1440
173	Arg Ile Ala Thr Gly Phe Ile Gly Asp His Pro His Leu Leu Gln Ala	
174	465 470 475 480	
176	cca cct gcg gat gat gag cag gga cgc atc ctg gat tac ttg gca gat	1488
177	Pro Pro Ala Asp Asp Glu Gln Gly Arg Ile Leu Asp Tyr Leu Ala Asp	
178	485 490 495	
180	gtc acc gtg aac aag cct cat ggt gtg cgt cca aag gat gtt gca gca	1536
181	Val Thr Val Asn Lys Pro His Gly Val Arg Pro Lys Asp Val Ala Ala	
182	500 505 510	
184	cca atc gat aag ctg ccc aac atc aag gat ctg cca ctg cca cgc ggt	1584
185	Pro Ile Asp Lys Leu Pro Asn Ile Lys Asp Leu Pro Leu Pro Arg Gly	
186	515 520 525	
188	tcc cgt gac cgc ctg aag cag ctt ggc cca gcc gcg ttt gct cgt gat	1632
189	Ser Arg Asp Arg Leu Lys Gln Leu Gly Pro Ala Ala Phe Ala Arg Asp	
190	530 535 540	
192	ctc cgt gag cag gac gca ctg gca gtt act gat acc acc ttc cgc gat	1680
193	Leu Arg Glu Gln Asp Ala Leu Ala Val Thr Asp Thr Thr Phe Arg Asp	
194	545 550 555 560	
196	gca cac cag tct ttg ctt gcg acc cga gtc cgc tca ttc gca ctg aag	1728
197	Ala His Gln Ser Leu Leu Ala Thr Arg Val Arg Ser Phe Ala Leu Lys	
198	565 570 575	
200	cct gcg gca gag gcc gtc gca aag ctg act cct gag ctt ttg tcc gtg	1776
201	Pro Ala Ala Glu Ala Val Ala Lys Leu Thr Pro Glu Leu Leu Ser Val	
202	580 585 590	
204	gag gcc tgg ggc ggc gcg acc tac gat gtg gcg atg cgt ttc ctc ttt	1824
205	Glu Ala Trp Gly Gly Ala Thr Tyr Asp Val Ala Met Arg Phe Leu Phe	
206	595 600 605	
208	gag gat ccg tgg gac agg ctc gac gag ctg cgc gag gcg atg ccg aat	1872
209	Glu Asp Pro Trp Asp Arg Leu Asp Glu Leu Arg Glu Ala Met Pro Asn	
210	610 615 620	
212	gta aac att cag atg ctg ctt cgc ggc cgc aac acc gtg gga tac acc	1920
213	Val Asn Ile Gln Met Leu Leu Arg Gly Arg Asn Thr Val Gly Tyr Thr	
214	625 630 635 640	
216	ccg tac cca gac tcc gtc tgc cgc gcg ttt gtt aag gaa gct gcc agc	1968
217	Pro Tyr Pro Asp Ser Val Cys Arg Ala Phe Val Lys Glu Ala Ala Ser	
218	645 650 655	
220	tcc ggc gtg gac atc ttc cgc atc ttc gac gcg ctt aac gac gtc tcc	2016

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221	Ser	Gly	Val	Asp	Ile	Phe	Arg	Ile	Phe	Asp	Ala	Leu	Asn	Asp	Val	Ser	
222				660					665				670				
224	cag	atg	cgt	cca	gca	atc	gac	gca	gtc	ctg	gag	acc	aac	acc	gcg	gta	2064
225	Gln	Met	Arg	Pro	Ala	Ile	Asp	Ala	Val	Leu	Glu	Thr	Asn	Thr	Ala	Val	
226			675					680					685				
228	gcc	gag	gtg	gct	atg	gct	tat	tct	ggt	gat	ctc	tct	gat	cca	aat	gaa	2112
229	Ala	Glu	Val	Ala	Met	Ala	Tyr	Ser	Gly	Asp	Leu	Ser	Asp	Pro	Asn	Glu	
230		690					695				700						
232	aag	ctc	tac	acc	ctg	gat	tac	tac	cta	aag	atg	gca	gag	gag	atc	gtc	2160
233	Lys	Leu	Tyr	Thr	Leu	Asp	Tyr	Tyr	Leu	Lys	Met	Ala	Glu	Glu	Ile	Val	
234	705					710				715						720	
236	aag	tct	ggc	gct	cac	att	ctg	gcc	att	aag	gat	atg	gct	ggt	ctg	ctt	2208
237	Lys	Ser	Gly	Ala	His	Ile	Leu	Ala	Ile	Lys	Asp	Met	Ala	Gly	Leu	Leu	
238				725					730				735				
240	cgc	cca	gct	gcg	gta	acc	aag	ctg	gtc	acc	gca	ctg	cgc	cgt	gaa	ttc	2256
241	Arg	Pro	Ala	Ala	Val	Thr	Lys	Leu	Val	Thr	Ala	Leu	Arg	Arg	Glu	Phe	
242				740					745				750				
244	gat	ctg	cca	gtg	cac	gtg	cac	acc	cac	gac	act	gcg	ggt	ggc	cag	ttg	2304
245	Asp	Leu	Pro	Val	His	Val	His	Thr	His	Asp	Thr	Ala	Gly	Gly	Gln	Leu	
246			755				760					765					
248	gct	acc	tac	ttt	gct	gca	gct	caa	gct	ggt	gca	gat	gct	gtt	gac	ggt	2352
249	Ala	Thr	Tyr	Phe	Ala	Ala	Gln	Ala	Gly	Ala	Asp	Ala	Val	Asp	Gly		
250		770				775				780							
252	gct	tcc	gca	cca	ctg	tct	ggc	acc	acc	tcc	cag	cca	tcc	ctg	tct	gcc	2400
253	Ala	Ser	Ala	Pro	Leu	Ser	Gly	Thr	Thr	Ser	Gln	Pro	Ser	Leu	Ser	Ala	
254	785				790					795						800	
256	att	gtt	gct	gca	ttc	gcg	cac	acc	cgt	cgc	gat	acc	ggt	ttg	agc	ctc	2448
257	Ile	Val	Ala	Ala	Phe	Ala	His	Thr	Arg	Arg	Asp	Thr	Gly	Leu	Ser	Leu	
258				805					810				815				
260	gag	gct	gtt	tct	gac	ctc	gag	ccg	tac	tgg	gaa	gct	gtg	cgc	gga	ctg	2496
261	Glu	Ala	Val	Ser	Asp	Leu	Glu	Pro	Tyr	Trp	Glu	Ala	Val	Arg	Gly	Leu	
262				820				825				830					
264	tac	ctg	cca	ttt	gag	tct	gga	acc	cca	ggc	cca	acc	ggt	cgc	gtc	tac	2544
265	Tyr	Leu	Pro	Phe	Glu	Ser	Gly	Thr	Pro	Gly	Pro	Thr	Gly	Arg	Val	Tyr	
266			835				840					845					
268	cgc	cac	gaa	atc	cca	ggc	gga	cag	ttg	tcc	aac	ctg	cgt	gca	cag	gcc	2592
269	Arg	His	Glu	Ile	Pro	Gly	Gly	Gln	Leu	Ser	Asn	Leu	Arg	Ala	Gln	Ala	
270		850				855				860							
272	acc	gca	ctg	ggc	ctt	gct	gat	cgc	ttc	gag	ctc	atc	gaa	gac	aac	tac	2640
273	Thr	Ala	Leu	Gly	Leu	Ala	Asp	Arg	Phe	Glu	Leu	Ile	Glu	Asp	Asn	Tyr	
274	865				870					875						880	
276	gca	gcc	gtt	aat	gag	atg	ctg	gga	cgc	cca	acc	aag	gtc	acc	cca	tcc	2688
277	Ala	Ala	Val	Asn	Glu	Met	Leu	Gly	Arg	Pro	Thr	Lys	Val	Thr	Pro	Ser	
278				885				890					895				
280	tcc	aag	gtt	gtt	ggc	gac	ctc	gca	ctc	cac	ctg	gtt	ggt	gcg	ggt	gta	2736
281	Ser	Lys	Val	Val	Gly	Asp	Leu	Ala	Leu	His	Leu	Val	Gly	Ala	Gly	Val	
282				900				905					910				
284	gat	cca	gca	gac	ttt	gct	gca	gac	cca	caa	aag	tac	gac	atc	cca	gac	2784
285	Asp	Pro	Ala	Asp	Phe	Ala	Ala	Asp	Pro	Gln	Lys	Tyr	Asp	Ile	Pro	Asp	

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290          930          935          940
292 tgg cca gaa cca ctg cgc acc cgc gca ctg gaa ggc cgc tcc gaa ggc      2880
293 Trp Pro Glu Pro Leu Arg Thr Arg Ala Leu Glu Gly Arg Ser Glu Gly
294 945          950          955          960
296 aag gca cct ctg acg gaa gtt cct gag gaa gag cag gcg cac ctc gac      2928
297 Lys Ala Pro Leu Thr Glu Val Pro Glu Glu Glu Gln Ala His Leu Asp
298          965          970          975
300 gct gat gat tcc aag gaa cgt cgc aac agc ctc aac cgc ctg ctg ttc      2976
301 Ala Asp Asp Ser Lys Glu Arg Arg Asn Ser Leu Asn Arg Leu Leu Phe
302          980          985          990
304 ccg aag cca acc gaa gag ttc ctc gag cac cgt cgc cgc ttc ggc aac      3024
305 Pro Lys Pro Thr Glu Glu Phe Leu Glu His Arg Arg Arg Phe Gly Asn
306          995          1000          1005
308 acc tct gcg ctg gat gat cgt gaa ttc ttc tac gga ctg gtc gag      3069
309 Thr Ser Ala Leu Asp Asp Arg Glu Phe Phe Tyr Gly Leu Val Glu
310          1010          1015          1020
312 ggc cgc gag act ttg atc cgc ctg cca gat gtg cgc acc cca ctg      3114
313 Gly Arg Glu Thr Leu Ile Arg Leu Pro Asp Val Arg Thr Pro Leu
314          1025          1030          1035
316 ctt gtt cgc ctg gat gcg atc tct gag cca gac gat aag ggt atg      3159
317 Leu Val Arg Leu Asp Ala Ile Ser Glu Pro Asp Asp Lys Gly Met
318          1040          1045          1050
320 cgc aat gtt gtg gcc aac gtc aac ggc cag atc cgc cca atg cgt      3204
321 Arg Asn Val Val Ala Asn Val Asn Gly Gln Ile Arg Pro Met Arg
322          1055          1060          1065
324 gtg cgt gac cgc tcc gtt gag tct gtc acc gca acc gca gaa aag      3249
325 Val Arg Asp Arg Ser Val Glu Ser Val Thr Ala Thr Ala Glu Lys
326          1070          1075          1080
328 gca gat tcc tcc aac aag ggc cat gtt gct gca cca ttc gct ggt      3294
329 Ala Asp Ser Ser Asn Lys Gly His Val Ala Ala Pro Phe Ala Gly
330          1085          1090          1095
332 gtt gtc act gtg act gtt gct gaa ggt gat gag gtc aag gct gga      3339
333 Val Val Thr Val Thr Val Ala Glu Gly Asp Glu Val Lys Ala Gly
334          1100          1105          1110
336 gat gca gtc gca atc atc gag gct atg aag atg gaa gca aca atc      3384
337 Asp Ala Val Ala Ile Ile Glu Ala Met Lys Met Glu Ala Thr Ile
338          1115          1120          1125
340 act gct tct gtt gac ggc aag att gaa cgc gtt gtg gtt cct gct      3429
341 Thr Ala Ser Val Asp Gly Lys Ile Glu Arg Val Val Val Pro Ala
342          1130          1135          1140
344 gca acg aag gtg gaa ggt ggc gac ttg atc gtc gtc gtt tcc taa      3474
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